

SEQUENCE LISTING

<110> Novak, Rodger
Toumanen, Elaine I.

<120> NOVEL ANTIBIOTICS AND METHODS OF USING THE SAME

<130> 1340-1-016 N

<140> UNASSIGNED

<141> 1999-05-05

<150> 09/073,541

<151> 1998-05-06

<160> 54

<170> PatentIn Ver. 2.0

<210> 1

<211> 75

<212> DNA

<213> bacterial

<400> 1

atgagaaagg aatttcacaa cgttttatct agtggtcagt tgcttgcaga caaaaggcca 60
gcaagagact ataat 75

<210> 2

<211> 25

<212> PRT

<213> bacterial

<400> 2

Met Arg Lys Glu Phe His Asn Val Leu Ser Ser Gly Gln Leu Leu Ala
1 5 10 15

Asp Lys Arg Pro Ala Arg Asp Tyr Asn
20 25

<210> 3

<211> 75

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 3
atgagaaagg aatttcacaa cgttttatct gctggtcagt tgcttcaga caaaaggcca 60
gcaagagact ataat 75

<210> 4
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 4
Met Lys Arg Glu Phe His Asn Val Leu Ser Ala Gly Gln Leu Leu Ala
1 5 10 15

Asp Lys Arg Pro Ala Arg Asp Tyr Asn
20 25

<210> 5
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 5
atgagaaagg aatttcacaa cgttttatct agtggtcagt tgcttcaga caaaaggcca 60
gcaagagacg ctaat 75

<210> 6
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 6
Met Arg Lys Glu Phe His Asn Val Leu Ser Ser Gly Gln Leu Leu Ala
1 5 10 15

Asp Lys Arg Pro Ala Arg Asp Ala Asn
20 25

<210> 7
<211> 42
<212> DNA
<213> bacterial

<400> 7
atgagaaagg aatttcacaa cgttttatct agtggtcagt tg 42

<210> 8
<211> 14
<212> PRT
<213> bacterial

<400> 8
Met Arg Lys Glu Phe His Asn Val Leu Ser Ser Gly Gln Leu
1 5 10

<210> 9
<211> 33
<212> DNA
<213> bacterial

<400> 9
cttgagaca aaaggccagc aagagactat aat 33

<210> 10
<211> 11
<212> PRT
<213> bacterial

<400> 10
Leu Ala Asp Lys Arg Pro Ala Arg Asp Tyr Asn
1 5 10

<210> 11
<211> 84
<212> DNA
<213> bacterial

<400> 11
atggaattta tgagaaagga atttcacaac gttttatcta gtggtcagtt gcttgagac 60
aaaaggccag caagagacta taat 84

<210> 12
<211> 28

<212> PRT
<213> bacterial

<400> 12

Met Glu Phe Met Arg Lys Glu Phe His Asn Val Leu Ser Ser Gly Gln
1 5 10 15

Leu Leu Ala Asp Lys Arg Pro Ala Arg Asp Tyr Asn
20 25

<210> 13
<211> 1329
<212> DNA
<213> bacterial

<400> 13

atgaaacgaa caggtttatt tgcaaagata tttatctata ctttctcgat atttagtggt 60
ctggttatct gccttcattt agctatttat tttctttttc cttcgactta tctgagtcac 120
cgtcaggaaa ccattgggtca aaaggcaaca gccattgccc agtccctaga agggaaagat 180
aggcagagta tcgagcaagt gtttagacttg tattcccaga ctagtgatat caaggggacc 240
gtcaaagggtg agatgaccga ggacaagtta gaagtcaagg acagtcttcc tctggacaca 300
gaccgccaga caacctctct ctttattgag gagcgcgagg tgaaaacgca agacggtggt 360
actatgattc tccagtttct agcttccatg gatttacaaa aggaagcgga gcaaatacagt 420
ctccagtttc ttccctatac cttgctggcc tcctttctga tttccctttt ggtggcctac 480
atctacgctc ggactattgt tgcaccgatt ttggaaatca agcgggtgac ccgtcggatg 540
atggacctgg attccaagt gcgattgctg gtggattcta aggatgagat aggtaatctc 600
aaggaacaaa tcaatagcct ctaccagcat ctcttgactg ttattgcgga cttgcatgaa 660
aagaatgaag ccattctcca gctggagaag atgaaggctg aattcctacg aggagcttct 720
catgaattga aaacaccgct ggctagtttg aaaatcctaa tcgaaaatat gagagagaat 780
atcggtcggt ataaggatag agaccagtat ctgggagttg cttgggggat tgtggatgaa 840
ctcaatcacc atgttctgca gatactttcc ctctcttctg tgcaggaatt gcgagatgat 900
agggaaacaa ttgacctcct ccagatgacg caaaatctgg tcaaagatta tgccttgcta 960
gccaaaggaaa gagagctcca gatagacaat agtttgacct atcagcaggc ttatctaaac 1020
ccatcagtta tgaagttgat tctttctaata ctcatcagca atgccattaa gcactctggt 1080
ccaggtggct tagttcgaat tggagaaaga gaaggagaac tttttatcga aaatagctgt 1140
agctcagagg aacaagaaaa actagcccag tctttttctg acaatgccag tcgcaaggct 1200
aaggggtctg gtatggggct ctttgtggtt aagagtctat tagaacatga aaaattagct 1260
tatcgtttcg agatggagga gaatagttta accttcttta tagattttcc aaaagtcgct 1320
caagactag 1329

<210> 14
<211> 442
<212> PRT
<213> bacterial

<400> 14

Met Lys Arg Thr Gly Leu Phe Ala Lys Ile Phe Ile Tyr Thr Phe Ser

0930594-050590

1	5	10	15
Ile Phe Ser Val Leu Val Ile Cys Leu His Leu Ala Ile Tyr Phe Leu	20	25	30
Phe Pro Ser Thr Tyr Leu Ser His Arg Gln Glu Thr Ile Gly Gln Lys	35	40	45
Ala Thr Ala Ile Ala Gln Ser Leu Glu Gly Lys Asp Arg Gln Ser Ile	50	55	60
Glu Gln Val Leu Asp Leu Tyr Ser Gln Thr Ser Asp Ile Lys Gly Thr	65	70	75
Val Lys Gly Glu Met Thr Glu Asp Lys Leu Glu Val Lys Asp Ser Leu	85	90	95
Pro Leu Asp Thr Asp Arg Gln Thr Thr Ser Leu Phe Ile Glu Glu Arg	100	105	110
Glu Val Lys Thr Gln Asp Gly Gly Thr Met Ile Leu Gln Phe Leu Ala	115	120	125
Ser Met Asp Leu Gln Lys Glu Ala Glu Gln Ile Ser Leu Gln Phe Leu	130	135	140
Pro Tyr Thr Leu Leu Ala Ser Phe Leu Ile Ser Leu Leu Val Ala Tyr	145	150	155
Ile Tyr Ala Arg Thr Ile Val Ala Pro Ile Leu Glu Ile Lys Arg Val	165	170	175
Thr Arg Arg Met Met Asp Leu Asp Ser Gln Val Arg Leu Arg Val Asp	180	185	190
Ser Lys Asp Glu Ile Gly Asn Leu Lys Glu Gln Ile Asn Ser Leu Tyr	195	200	205
Gln His Leu Leu Thr Val Ile Ala Asp Leu His Glu Lys Asn Glu Ala	210	215	220
Ile Leu Gln Leu Glu Lys Met Lys Val Glu Phe Leu Arg Gly Ala Ser	225	230	235
His Glu Leu Lys Thr Pro Leu Ala Ser Leu Lys Ile Leu Ile Glu Asn	245	250	255
Met Arg Glu Asn Ile Gly Arg Tyr Lys Asp Arg Asp Gln Tyr Leu Gly			

270

Phe Ile Asp Phe Pro Lys Val Val Gln Asp
435 440

```
<210> 15
<211> 657
<212> DNA
<213> bacterial
```

<400> 15						
atgaaaattt	taattgtaga	agatgaagag	atgatccgtg	aggggggtcag	tgattatttg	60
acggattgtg	gctatgaaac	tattgaggca	gcggacggtc	aggaagctct	ggagcaattt	120
tctagctatg	aggtggccct	ggttttactg	gatatccaga	tgcccaagct	caacggctta	180
gaagtcctag	ctgagattcg	taaaaccagt	caggttcctg	tcttgatgtt	gacagctttt	240
caagatgagg	aatacaagat	gagtgccttt	gcctcttttg	cagatggcta	tctggaaaaa	300
cctttctccc	tctccctttt	aaaagtgagg	gtggacgcga	ttttcaagcg	ctactacgat	360

acaggacgaa tcttttctta caaggatacc aaggtggact ttgaaagcta cagtgcgaagc 420
 ctgcgaggtc aagaagtgcc tatcaatgcc aaagagttgg aaattctgga ctatctagtg 480
 aaaaatgaag gccgggcctt gactcgatct cagattatcg atgccgtctg gaaagcgaca 540
 gatgaggttc cctttgaccg tggtattgat gtttatatca aggaattgcg gaaaaagcta 600
 gacttggatt gtatcctcac tgtgcgcaat gttggttata aattggagcg aaaatga 657

<210> 16
 <211> 218
 <212> PRT
 <213> bacterial

<400> 16

Met	Lys	Ile	Leu	Ile	Val	Glu	Asp	Glu	Glu	Met	Ile	Arg	Glu	Gly	Val
1				5					10					15	
Ser	Asp	Tyr	Leu	Thr	Asp	Cys	Gly	Tyr	Glu	Thr	Ile	Glu	Ala	Ala	Asp
			20					25					30		
Gly	Gln	Glu	Ala	Leu	Glu	Gln	Phe	Ser	Ser	Tyr	Glu	Val	Ala	Leu	Val
		35					40					45			
Leu	Leu	Asp	Ile	Gln	Met	Pro	Lys	Leu	Asn	Gly	Leu	Glu	Val	Leu	Ala
	50					55					60				
Glu	Ile	Arg	Lys	Thr	Ser	Gln	Val	Pro	Val	Leu	Met	Leu	Thr	Ala	Phe
65					70					75				80	
Gln	Asp	Glu	Glu	Tyr	Lys	Met	Ser	Ala	Phe	Ala	Ser	Leu	Ala	Asp	Gly
				85					90					95	
Tyr	Leu	Glu	Lys	Pro	Phe	Ser	Leu	Ser	Leu	Leu	Lys	Val	Arg	Val	Asp
			100					105					110		
Ala	Ile	Phe	Lys	Arg	Tyr	Tyr	Asp	Thr	Gly	Arg	Ile	Phe	Ser	Tyr	Lys
		115					120					125			
Asp	Thr	Lys	Val	Asp	Phe	Glu	Ser	Tyr	Ser	Ala	Ser	Leu	Ala	Gly	Gln
	130					135					140				
Glu	Val	Pro	Ile	Asn	Ala	Lys	Glu	Leu	Glu	Ile	Leu	Asp	Tyr	Leu	Val
145					150					155				160	
Lys	Asn	Glu	Gly	Arg	Ala	Leu	Thr	Arg	Ser	Gln	Ile	Ile	Asp	Ala	Val
				165					170					175	
Trp	Lys	Ala	Thr	Asp	Glu	Val	Pro	Phe	Asp	Arg	Val	Ile	Asp	Val	Tyr
			180					185					190		

0030594.05050

Ile Lys Glu Leu Arg Lys Lys Leu Asp Leu Asp Cys Ile Leu Thr Val
 195 200 205

Arg Asn Val Gly Tyr Lys Leu Glu Arg Lys
 210 215

<210> 17
 <211> 648
 <212> DNA
 <213> bacterial

<400> 17
 atgactttat tacaattaca agatgttacc taccgttata agaatactgc tgaagcagtc 60
 ctatatcaga tcaattataa ttttgaaccc ggaaaatttt acagtattat tggggagtca 120
 ggagcaggaa aatccacact cttgtcccta cttgctggtc tagatagtcc tgttgaaggt 180
 tctatccttt ttcaaggaga ggatattcgt aagaagggtc attcttacca tcgcatgcac 240
 catatttccc tgggtctttca aaattataac ttgatagatt atctttctcc gctggaaaat 300
 atccgatttg tcaacaaaaa ggcaagcaag aatacacttc ttgagcttgg tttggatgaa 360
 agccagatca agcggaatgt tctccagtta tcaggtggtc aacagcaacg tgttgccatt 420
 gctcgcagtt tgggtctcaga agctccagtt attctagctg atgagccaac aggaaatctg 480
 gatcctaata ctgctggaga tattgtcgaa ctactcaaat cacttgccca gaaaacaggt 540
 aaatgtgtga ttgtcgtaac tcacagtaaa gaagtggcac aagcgtcaga tattacactt 600
 gaattaaagg ataagaaact gactgaaacg cgcaatacta gtaaataa 648

<210> 18
 <211> 215
 <212> PRT
 <213> bacterial

<400> 18
 Met Thr Leu Leu Gln Leu Gln Asp Val Thr Tyr Arg Tyr Lys Asn Thr
 1 5 10 15
 Ala Glu Ala Val Leu Tyr Gln Ile Asn Tyr Asn Phe Glu Pro Gly Lys
 20 25 30
 Phe Tyr Ser Ile Ile Gly Glu Ser Gly Ala Gly Lys Ser Thr Leu Leu
 35 40 45
 Ser Leu Leu Ala Gly Leu Asp Ser Pro Val Glu Gly Ser Ile Leu Phe
 50 55 60
 Gln Gly Glu Asp Ile Arg Lys Lys Gly Tyr Ser Tyr His Arg Met His
 65 70 75 80
 His Ile Ser Leu Val Phe Gln Asn Tyr Asn Leu Ile Asp Tyr Leu Ser
 85 90 95

Pro Leu Glu Asn Ile Arg Leu Val Asn Lys Lys Ala Ser Lys Asn Thr
 100 105 110
 Leu Leu Glu Leu Gly Leu Asp Glu Ser Gln Ile Lys Arg Asn Val Leu
 115 120 125
 Gln Leu Ser Gly Gly Gln Gln Gln Arg Val Ala Ile Ala Arg Ser Leu
 130 135 140
 Val Ser Glu Ala Pro Val Ile Leu Ala Asp Glu Pro Thr Gly Asn Leu
 145 150 155 160
 Asp Pro Lys Thr Ala Gly Asp Ile Val Glu Leu Leu Lys Ser Leu Ala
 165 170 175
 Gln Lys Thr Gly Lys Cys Val Ile Val Val Thr His Ser Lys Glu Val
 180 185 190
 Ala Gln Ala Ser Asp Ile Thr Leu Glu Leu Lys Asp Lys Lys Leu Thr
 195 200 205
 Glu Thr Arg Asn Thr Ser Lys
 210 215

<210> 19
 <211> 1380
 <212> DNA
 <213> bacterial

<400> 19
 atgttacaca acgcatttgc ctatgtttaca aggaagtttt tcaaatacgat tgtcatcttc 60
 ctgattattc tctcatggc gagcttgagt ttggtcggct tgtcaatcaa gggagctact 120
 gccaaaggctt ctcaggagac ctttaaaaat atcaccaata gcttctccat gcaaatacaat 180
 cgtcgcgtca accaaggaac gcctcgtggt gctgggaata tcaagggtga agacatcaaa 240
 aaaatcaccg aaaacaaggc cattgagtct tatgtcaaac gtatcaacgc tatcgagat 300
 ttgactggat atgacctgat tgaaacgcca gaaaccaaga agaattctac tgetgatcgt 360
 gccaaagcgtt ttggaagtag cttgatgatt acagggtgtca atgactcctc taaagaagac 420
 aagtttgtct ctggttctta taaactagtc gaaggagagc acttaaccaa cgacgacaag 480
 gataaaatcc tcttgacaa ggacttggca gccaaacacg gctggaaagt aggggacaag 540
 gttaaactgg actctaatat ctacgatgca gataatgaaa aaggagccaa ggaacagtt 600
 gaagtgcaca tcaagggact ctttgatggt cataataagt cagcagtaac ctactcaca 660
 gaactttacg aaaacacagc tattacagac attcacactg ctgcaaaact ttatggatac 720
 acagaagaca cagccattta tggggacgca accttctttg taacagcaga caagaacttg 780
 gatgatgtta tgaaagagtt gaatggcatc agtggatatca actggaagag ctacacactc 840
 gtcaagagct cctctaacta ccagctctt gagcaatcta tctctggtat gtacaagatg 900
 gccaacctcc tcttctgggg tagcttgagc ttctcagttc tcctccttgc cctcttgctc 960

agcctttgga tcaacgcccg tcgcaaggaa gtgggaattc tcctctctat cggcctcaag 1020
caggcaagta tcttgggtca attcatcacc gaatctatct tgattgctat ccctgctcta 1080
gtttctgctt acttcctagc taattacact gcccgtgcaa ttggaaacac tgtccttgcc 1140
aatgtgactt caggtgttgc caaacaggct agtaaggcgg ctcaagcctc taaccttggt 1200
ggtggtgcag aagtagatgg ctttagcaag accttgtcga gcctagacat ttccattcag 1260
acatcagact ttatcatcat ttttgtcctt gccttggttc tagtggttct cgttatggcg 1320
cttgcttcaa gcaatctcct tagaaaacaa ccaaagagc tcttgctgga tgggtgaataa 1380

<210> 20

<211> 459

<212> PRT

<213> bacterial

<400> 20

Met Leu His Asn Ala Phe Ala Tyr Val Thr Arg Lys Phe Phe Lys Ser
1 5 10 15

Ile Val Ile Phe Leu Ile Ile Leu Leu Met Ala Ser Leu Ser Leu Val
20 25 30

Gly Leu Ser Ile Lys Gly Ala Thr Ala Lys Ala Ser Gln Glu Thr Phe
35 40 45

Lys Asn Ile Thr Asn Ser Phe Ser Met Gln Ile Asn Arg Arg Val Asn
50 55 60

Gln Gly Thr Pro Arg Gly Ala Gly Asn Ile Lys Gly Glu Asp Ile Lys
65 70 75 80

Lys Ile Thr Glu Asn Lys Ala Ile Glu Ser Tyr Val Lys Arg Ile Asn
85 90 95

Ala Ile Gly Asp Leu Thr Gly Tyr Asp Leu Ile Glu Thr Pro Glu Thr
100 105 110

Lys Lys Asn Leu Thr Ala Asp Arg Ala Lys Arg Phe Gly Ser Ser Leu
115 120 125

Met Ile Thr Gly Val Asn Asp Ser Ser Lys Glu Asp Lys Phe Val Ser
130 135 140

Gly Ser Tyr Lys Leu Val Glu Gly Glu His Leu Thr Asn Asp Asp Lys
145 150 155 160

Asp Lys Ile Leu Leu His Lys Asp Leu Ala Ala Lys His Gly Trp Lys
165 170 175

Val Gly Asp Lys Val Lys Leu Asp Ser Asn Ile Tyr Asp Ala Asp Asn

190

Val Leu Val Val Leu Val Met Ala Leu Ala Ser Ser Asn Leu Leu Arg

435

440

445

Lys Gln Pro Lys Glu Leu Leu Asp Gly Glu
450 455

<210> 21
<211> 1278
<212> DNA
<213> bacterial

<400> 21
atgaatccaa tccaaagatc ttgggcttat gtcagcagaa agcgactgag aagttttatt 60
ttatttctga ttttattggt cttattggcc ggaatttcag cctgtttgac tctgatgaag 120
tccaacaaaa cagtagaaaag caatctttat aaatcactca atacatcttt ttctattaag 180
aagatagaga atggtcagac attcaagttg tcagacctag catctgtaag caagattaag 240
gggctggaaa atgtctctcc tgaacttgag acggtcgcaa aactaaaaga caaggaagca 300
gtgactggcg agcagagcgt ggagcgtgat gatttatcag ctgcagacaa taacttggtt 360
agcttaacgg ctcttgagga ttcattccaag gatgtaacct ttaccagttc ggctttcaat 420
ctaaaagaag ggcgacacct tcaaaaaggg gattccaaga aaatccttat ccacgaagaa 480
ttggctaaga agaacggtct ttcgcttcat gacaagattg gcttggatgc tggtcagtct 540
gaatctggaa aaggacaaac agtagagttt gagattatcg gcatcttttc tggtaaaaaa 600
caagagaaat tcacaggctt gtcttctgac ttcagtgaag atcaagtctt tacagactat 660
gaaagtagcc aaaccctttt gggcaatagt gaagctcaag tcagtgcagc acgcttctat 720
gtagaaaatc ctaaggaaat ggacggactc atgaagcagg tagaaaactt ggcttggaa 780
aatcaaggct accaagtcga aaaggaaaac aaggcctttt aacaaatcaa agactcagtt 840
gcaactttcc aaaccttcct gaccatcttc ctttatggga tgttgatagc aggagctgga 900
gccttaattc tggttttgtc tctctggttg agagaacggg tctatgaagt ggggatttta 960
cttgcaactg gaaaaggcaa gagctcgatc ttcctacaat tctgtttaga ggtagttttg 1020
gtatctcttg gagctttgct tccagcattt gttgcaggaa acgcaatcac aacttaccta 1080
ctccaaactc tactagcaag tggagatcag gcaagcttac aagatacact agccaaagca 1140
agcagtttat caactagcat cttatctttt gcagaatcct atgtttttct agttctgctt 1200
agttgcttat ctgtagccct ttgtttccta ttcttattta gaaaatcacc gaaagaaatt 1260
ttatcatcta ttagttaa 1278

<210> 22
<211> 425
<212> PRT
<213> bacterial

<400> 22
Met Asn Pro Ile Gln Arg Ser Trp Ala Tyr Val Ser Arg Lys Arg Leu
1 5 10 15
Arg Ser Phe Ile Leu Phe Leu Ile Leu Leu Val Leu Leu Ala Gly Ile
20 25 30
Ser Ala Cys Leu Thr Leu Met Lys Ser Asn Lys Thr Val Glu Ser Asn

45

Ile Phe Leu Tyr Gly Met Leu Ile Ala Gly Ala Gly Ala Leu Ile Leu

290

295

300

Val Leu Ser Leu Trp Leu Arg Glu Arg Val Tyr Glu Val Gly Ile Leu
305 310 315 320

Leu Ala Leu Gly Lys Gly Lys Ser Ser Ile Phe Leu Gln Phe Cys Leu
325 330 335

Glu Val Val Leu Val Ser Leu Gly Ala Leu Leu Pro Ala Phe Val Ala
340 345 350

Gly Asn Ala Ile Thr Thr Tyr Leu Leu Gln Thr Leu Leu Ala Ser Gly
355 360 365

Asp Gln Ala Ser Leu Gln Asp Thr Leu Ala Lys Ala Ser Ser Leu Ser
370 375 380

Thr Ser Ile Leu Ser Phe Ala Glu Ser Tyr Val Phe Leu Val Leu Leu
385 390 395 400

Ser Cys Leu Ser Val Ala Leu Cys Phe Leu Phe Leu Phe Arg Lys Ser
405 410 415

Pro Lys Glu Ile Leu Ser Ser Ile Ser
420 425

<210> 23

<211> 1407

<212> DNA

<213> bacterial

<400> 23

atgccgaacg gcacgtatgg tgggtgtgaga ggggctagag attatcccct actcgatatt 60
tttttttcgt atttcataaa tatttcatat ttgggtttta taatagtctt acaaatatgg 120
aggtgacaaa tgaatccaat ccaaagatct tgggcttatg tcagcagaaa gcgactgaga 180
agttttatct tatttctgat tttattggtc ttattggccg gaatttcagc ctgtttgact 240
ctgatgaagt ccaacaaaac agtagaaagc aatctttata aatcactcaa tacatctttt 300
tctattaaga agatagagaa tggtcagaca ttcaagttgt cagacctagc atctgtaagc 360
aagattaagg ggctggaaaa tgtctctcct gaacttgaga cggtcgcaaa actaaaagac 420
aaggaagcag tgactggcga gcagagcgtg gagcgtgatg atttatcagc tgcagacaat 480
aacttggtta gcttaacggc tcttgaggat tcatccaagg atgtaacctt taccagttcg 540
gctttcaatc taaaagaagg gcgacacctt caaaaagggg attccaagaa aatccttatc 600
cacgaagaat tggctaagaa gaacggtctt tcgcttcattg acaagattgg cttggatgct 660
ggtcagtctg aatctggaaa aggacaaaca gttagagttt agattatcgg catcttttct 720
ggtaaaaaac aagagaaatt cacaggcttg tcttctgact tcagtgaata tcaagtcttt 780
acagactatg aaagtagcca aacccttttg ggcaatagtg aagctcaagt cagtgcagca 840
cgcttctatg tagaaaatcc taaggaaatg gacggactca tgaagcaggt agaaaacttg 900

gccttggaat atcaaggcta ccaagtcgaa aaggaaaaca aggcttttga acaaatcaaa 960
gactcagttg caactttcca aaccttcctg accatcttcc tttatgggat gttgatagca 1020
ggagctggag ccttaattct gggtttgtct ctctggttga gagaacgggt ctatgaagtg 1080
gggattttac ttgcacttgg aaaaggcaag agctcgatct tcctacaatt ctgttttagag 1140
gtagttttgg tatctcttgg agctttgctt ccagcatttg ttgcaggaaa cgcaatcaca 1200
acttacctac tccaaactct actagcaagt ggagatcagg caagcttaca agatacacta 1260
gccaaagcaa gcagttttatc aactagcatc ttatcttttg cagaatccta tgtttttcta 1320
gttctgctta gttgcttata tgtagccctt tgtttcctat tcttatttag aaaatcaccg 1380
aaagaaattt tatcatctat tagttaa 1407

<210> 24
<211> 425
<212> PRT
<213> bacterial

<400> 24

Met Asn Pro Ile Gln Arg Ser Trp Ala Tyr Val Ser Arg Lys Arg Leu
1 5 10 15

Arg Ser Phe Ile Leu Phe Leu Ile Leu Leu Val Leu Leu Ala Gly Ile
20 25 30

Ser Ala Cys Leu Thr Leu Met Lys Ser Asn Lys Thr Val Glu Ser Asn
35 40 45

Leu Tyr Lys Ser Leu Asn Thr Ser Phe Ser Ile Lys Lys Ile Glu Asn
50 55 60

Gly Gln Thr Phe Lys Leu Ser Asp Leu Ala Ser Val Ser Lys Ile Lys
65 70 75 80

Gly Leu Glu Asn Val Ser Pro Glu Leu Glu Thr Val Ala Lys Leu Lys
85 90 95

Asp Lys Glu Ala Val Thr Gly Glu Gln Ser Val Glu Arg Asp Asp Leu
100 105 110

Ser Ala Ala Asp Asn Asn Leu Val Ser Leu Thr Ala Leu Glu Asp Ser
115 120 125

Ser Lys Asp Val Thr Phe Thr Ser Ser Ala Phe Asn Leu Lys Glu Gly
130 135 140

Arg His Leu Gln Lys Gly Asp Ser Lys Lys Ile Leu Ile His Glu Glu
145 150 155 160

Leu Ala Lys Lys Asn Gly Leu Ser Leu His Asp Lys Ile Gly Leu Asp
165 170 175

Ala	Gly	Gln	Ser	Glu	Ser	Gly	Lys	Gly	Gln	Thr	Val	Glu	Phe	Glu	Ile	
			180					185					190			
Ile	Gly	Ile	Phe	Ser	Gly	Lys	Lys	Gln	Glu	Lys	Phe	Thr	Gly	Leu	Ser	
		195					200					205				
Ser	Asp	Phe	Ser	Glu	Asn	Gln	Val	Phe	Thr	Asp	Tyr	Glu	Ser	Ser	Gln	
	210					215					220					
Thr	Leu	Leu	Gly	Asn	Ser	Glu	Ala	Gln	Val	Ser	Ala	Ala	Arg	Phe	Tyr	
225					230					235					240	
Val	Glu	Asn	Pro	Lys	Glu	Met	Asp	Gly	Leu	Met	Lys	Gln	Val	Glu	Asn	
				245					250						255	
Leu	Ala	Leu	Glu	Asn	Gln	Gly	Tyr	Gln	Val	Glu	Lys	Glu	Asn	Lys	Ala	
			260					265						270		
Phe	Glu	Gln	Ile	Lys	Asp	Ser	Val	Ala	Thr	Phe	Gln	Thr	Phe	Leu	Thr	
		275					280						285			
Ile	Phe	Leu	Tyr	Gly	Met	Leu	Ile	Ala	Gly	Ala	Gly	Ala	Leu	Ile	Leu	
	290					295					300					
Val	Leu	Ser	Leu	Trp	Leu	Arg	Glu	Arg	Val	Tyr	Glu	Val	Gly	Ile	Leu	
305					310					315					320	
Leu	Ala	Leu	Gly	Lys	Gly	Lys	Ser	Ser	Ile	Phe	Leu	Gln	Phe	Cys	Leu	
				325					330					335		
Glu	Val	Val	Leu	Val	Ser	Leu	Gly	Ala	Leu	Leu	Pro	Ala	Phe	Val	Ala	
			340					345						350		
Gly	Asn	Ala	Ile	Thr	Thr	Tyr	Leu	Leu	Gln	Thr	Leu	Leu	Ala	Ser	Gly	
		355					360					365				
Asp	Gln	Ala	Ser	Leu	Gln	Asp	Thr	Leu	Ala	Lys	Ala	Ser	Ser	Leu	Ser	
	370					375					380					
Thr	Ser	Ile	Leu	Ser	Phe	Ala	Glu	Ser	Tyr	Val	Phe	Leu	Val	Leu	Leu	
385					390					395					400	
Ser	Cys	Leu	Ser	Val	Ala	Leu	Cys	Phe	Leu	Phe	Leu	Phe	Arg	Lys	Ser	
				405					410					415		
Pro	Lys	Glu	Ile	Leu	Ser	Ser	Ile	Ser								
			420					425								

<210> 25
 <211> 8900
 <212> DNA
 <213> bacterial

<400> 25

```

gataagtttg tagcagctat ggatgaagat tttaatgctg ccaacggtat cacagttgtc 60
tttgaaatgg ccaaattggat caactcaggg aactatgatg caagtgtcaa gcaagctctt 120
gcagatatgt tagaaatttt tggaattgtc tttgttgagg aagttttgga tgcagagatt 180
gaagacttga ttcaaaaacg ccaagaggcg cgtgccaatc gtgactttgc gacagcagac 240
caaatccgtg accaattggg tactcaagga attaagctcc ttgataccaa ggatggagtg 300
agggtggacac gtgattgatg tcaatctcat taacgggatt gcgctagcct ttgaggggga 360
tgcggtgtat tctatgtata ttccgctgca cctcatcctc aaaggatatga ccaaacccaa 420
taaaactccat caagaagcaa ctaagtacgt gtcagccaag gctcaggctc gcctgattgc 480
tctcatgttg gaggagcagg tcctaacgga aaaagaagaa gaaatctaca aacgtggccg 540
caataccaat agccacacaa aggctaaaaa tgcagatgtc gtgacttatt gtatgtccac 600
gggatttgaa gcggttatgg gctatctcca tatgactgag aatctggaac gtcttgagag 660
tttggtttca tgggtgcatcc aaaaagtgga gggctagaac atgagggcaa aagaactaca 720
agactggttt cctgaggctc ggatttcaga ccaaccagta gagaaagagg gctatctcac 780
gctcccttta gcttctcagc agtggatttt gctggaggaa gctgggctca gcgagcgtga 840
aaagcagttg gttgcccttt tgaccagca ggagcaggct cgttcgctaa acccttggtg 900
ttcctatctg gttgagggca agggacaggc accgcaagtt tttaaaaaga ttcagttggg 960
ttattgccat ctttcttatt ttcagcagga aaatctggct tcttggttag atatgatgcg 1020
gactcttttt ccgaattgtc agacagtgtc acaggtcgga gctcaggatt atgttttcgt 1080
gcttcaacaa gacaaatata cttctgtaag agatatttta agtgatacga ttgaagcggg 1140
tgagtatgac tttggacttc gtctttctat catgttgggt caggtttggg ctgagacggg 1200
acatcaagcc ctatcagact taatcaaagc tgagcgggat ttgttcaaga catggtggcg 1260
tcagggtcac caaggtgttc atactttttc tcagctctat ctttgagta tgggagaaaag 1320
actcgtggac ttgaagccaa tcaaggaatg tctacaccag atgatttttg atcaagatca 1380
gattcaggaa atcattctct ctctttggga aaatagtgtc gttctcacta aaacagccca 1440
gcaactctat ctgcaccgca attctctcca atacaagatt gataaatggg aagagttgac 1500
agggcttcag ttgaaagagt tgaccgacct gaccttgtgt tatcaattga ttttaggttc 1560
tttgtcaact atagttaggt tgtaaagaag ttaatatattg gagaagagga ttgccatctt 1620
ctccattttt atgtgcagag ttatagtggc ttgatgctgg gaaagtacac tgtgactgct 1680
aaaacattcc tagaagctgc tttgatttcc ctaatctatt tatgcaaatt ttatgttatt 1740
ttactataac agttgttgct aagccaaata atagtgggga agttcattta gacgtaagca 1800
ttgaagataa tcaggagggt agtgggtata atttcagttc tgtttcaagt agctcacaaa 1860
cagctaaata tgaagggaact gtttataata acaattcatc attatatata acgattgata 1920
aaacgtctga tgcaacagct cttttgaaat taaagttgaa taatgttgat aatcaacctg 1980
ctactgaagt tcctagttca ggaattactg taaaattaaa tgctaaagat aatgctggaa 2040
actggacaag tgcttcgaat aaaaaagaag taacagtaaa aattgtttct gctaaaccga 2100
catatccaga caaaatctta gtgaaaaatc ctgataatat aaaagatata gaaaaaatgc 2160
cattattgaa aaattgaaag aggcaaataa aaatcatcca gcaggagctc caacctttgc 2220
taaaggtgaa ggagagcatg caaatgatat tgtagcaact tattcagatg gtacaactta 2280
ttatgtaccg ttaaatgatg tgacaaaata tgcgaggtag tggctgtacc actcacttat 2340
tcacctcccc gtgatttgta gtagtgatag gttttctcac tattattata aaacaaaata 2400

```

aagatcacaa	cactttttca	ttctgtgttg	tgccttgagt	gaaacgaaag	gaatgaatta	2460
taaatatgaa	aagtatagtc	actagcatag	atgagcgctt	gcgtactcgc	ctacgagtga	2520
ttatctggaa	gcaatggaag	aagaaatcga	gacgattatg	gggattgctt	aagttagggg	2580
ttcctaaatg	gatagcagat	aaggtatctg	gctggggcga	ccactatcaa	ttatagtaaa	2640
atgaaataag	aataggacga	attgttcagg	acagtcaaat	cgattttctaa	caatatttta	2700
gaagtagagg	tgtactattc	tagtttcaat	ctactatagt	agctcagaag	tcggtagtta	2760
aacgtgctat	atcaaaacca	gtccttgaaa	aacgtggact	ggtttcgtgt	ttggattatt	2820
accttgaacg	acatgcgtta	aaagttagtt	gaaccgccgt	atgccgaacg	gcacgtatgg	2880
tgggtgtgaga	ggggctagag	attatcccct	actcgatatt	tttttttcgt	atttcataaa	2940
tatttcatat	ttgggtttta	taatagtctt	acaaatatgg	aggtgacaaa	tgaatccaat	3000
ccaaagatct	tgggcttatg	tcagcagaaa	gcgactgaga	agttttattt	tattttctgat	3060
tttattggtc	ttattggccg	gaatttcagc	ctgtttgact	ctgatgaagt	ccaacaaaaac	3120
agtagaaaagc	aatctttata	aatcactcaa	tacatctttt	tctattaaga	agatagagaa	3180
tggtcagaca	ttcaagttgt	cagacctagc	atctgtaagc	aagattaagg	ggctggaaaa	3240
tgtctctcct	gaacttgaga	cggtcgcaaa	actaaaagac	aaggaagcag	tgactggcga	3300
gcagagcgtg	gagcgtgatg	atztatcagc	tgacagacaat	aacttggtta	gcttaacggc	3360
tcttgaggat	tcatccaagg	atgtaacctt	taccagttcg	gctttcaatc	taaaagaagg	3420
gcgacacctt	caaaaagggg	attccaagaa	aatccttatc	cacgaagaat	tggctaagaa	3480
gaacggctctt	tcgcttcatg	acaagattgg	cttggatgct	ggtcagtcctg	aatctggaaa	3540
aggacaaaca	gtagagtttg	agattatcgg	catcttttct	ggtaaaaaac	aagagaaatt	3600
cacaggcttg	tcttctgact	tcagtgaaaa	tcaagtcttt	acagactatg	aaagtagcca	3660
aacccttttg	ggcaatagtg	aagctcaagt	cagtgcagca	cgcttctatg	tagaaaatcc	3720
taaggaaatg	gacggactca	tgaagcaggt	agaaaacttg	gccttgghaa	atcaaggcta	3780
ccaagtcgaa	aaggaaaaca	aggcttttga	acaaatcaaa	gactcagttg	caactttcca	3840
aaccttcctg	accatcttcc	tttatgggat	gttgatagca	ggagctggag	ccttaattct	3900
ggttttgtct	ctctggttga	gagaacgggt	ctatgaagtg	gggattttac	ttgcacttgg	3960
aaaaggcaag	agctcgatct	tctacaatt	ctgttttagag	gtagttttgg	tatctcttgg	4020
agctttgctt	ccagcatttg	ttgcaggaaa	cgcaatcaca	acttacctac	tccaaactct	4080
actagcaagt	ggagatcagg	caagcttaca	agatacacta	gccaaagcaa	gcagttttatc	4140
aactagcatc	ttatcttttg	cagaatccta	tgtttttcta	gttctgttta	gttgcttatc	4200
tgtagccctt	tgtttcctat	tcttatttag	aaaatcaccg	aaagaaattt	tatcatctat	4260
tagttaagaa	ggagaaatca	tgactttatt	acaattacaa	gatgttacct	accgtttataa	4320
gaatactgct	gaagcagtc	tatatcagat	caattataat	tttgaaccgg	gaaaatttta	4380
cagtattatt	ggggagtcag	gagcaggaaa	atccacactc	ttgtccctac	ttgctgggtct	4440
agatagtcct	gttgaagggt	ctatcctttt	tcaaggagag	gatattcgta	agaagggtcta	4500
ttcttaccat	cgcatgcacc	atatttcctt	ggtctttcaa	aattataact	tgatagatta	4560
tctttctccg	ctggaaaata	tccgattggg	caacaaaaag	gcaagcaaga	atacacttct	4620
tgagcttggg	ttggatgaaa	gccagatcaa	gcggaatgtt	ctccagttat	caggtgggtca	4680
acagcaacgt	gttgccattg	ctcgcagttt	ggtctcagaa	gctccagtta	ttctagctga	4740
tgagccaaca	ggaaatctgg	atcctaaaac	tgctggagat	attgtcgaac	tactcaaatc	4800
acttgcccag	aaaacaggta	aatgtgtgat	tgtcgttaact	cacagtaaa	aagtggcaca	4860
agcgtcagat	attacacttg	aattaaaagg	taagaaactg	actgaaacgc	gcaatactag	4920
taaataattt	gagcttattt	taatagaatg	attaaaacaa	aatctagaaa	gggaatctat	4980
gttacacaac	gcatttgcc	atgttacaa	gaagtttttc	aaatcgattg	tcattcttct	5040
gattattctc	ctcatggcga	gcttgagttt	ggtcggcttg	tcaatcaagg	gagctactgc	5100
caaggcttct	caggagacct	ttaaaaaat	caccaatagc	ttctccatgc	aaatcaatcg	5160
tcgcgtcaac	caaggaacgc	ctcgtgggtg	tgggaatatc	aagggtgaag	acatcaaaaa	5220
aatcacccgaa	aacaaggcca	ttgagtcctt	tgtcaaacgt	atcaacgcta	tcggagattt	5280

gactggatat	gacctgattg	aaacgccaga	aaccaagaag	aatctcactg	ctgacgtgc	5340
caagcgtttt	ggaagtagct	tgatgattac	aggtgtcaat	gactcctcta	aagaagacaa	5400
gtttgtctct	ggttcttata	aactagtcga	aggagagcac	ttaaccaacg	acgacaagga	5460
taaaatcctc	ttgcacaagg	acttggcagc	caaacacggc	tggaaagtag	gggacaaggt	5520
taaactggac	tctaatatct	acgatgcaga	taatgaaaaa	ggagccaagg	aaacagttga	5580
agtgacaatc	aagggactct	ttgatgggtca	taataagtca	gcagtaacct	actcacaaga	5640
actttacgaa	aacacagcta	ttacagacat	tcacactgct	gcaaaacttt	atggatacac	5700
agaagacaca	gccatttatg	gggacgcaac	cttctttgta	acagcagaca	agaacttgga	5760
tgatgttatg	aaagagttga	atggcatcag	tggtatcaac	tggagagact	acacactcgt	5820
caagagctcc	tctaactacc	cagctcttga	gcaatctatc	tctggtatgt	acaagatggc	5880
caacctcctc	ttctggggta	gcttgagctt	ctcagttctc	ctccttgccc	tcttgctcag	5940
cctttggatc	aacgcccgtc	gcaaggaagt	gggaattctc	ctctctatcg	gcctcaagca	6000
ggcaagtatc	ttgggtcaat	tcatacccca	atctatcttg	attgctatcc	ctgctctagt	6060
ttctgcttac	ttcctagcta	attacactgc	ccgtgcaatt	ggaaacactg	tccttgccaa	6120
tgtgacttca	ggtgttgcca	aacaggctag	taaggcggct	caagcctcta	accttgggtg	6180
tggtgcagaa	gtagatggct	ttagcaagac	cttgctcgagc	ctagacattt	ccattcagac	6240
atcagacttt	atcatcattt	ttgtccttgc	cttggttcta	gtggttctcg	ttatggcgct	6300
tgcttcaagc	aatctcctta	gaaaacaacc	aaaagagctc	ttgctggatg	gtgaataaat	6360
ttgaaaaaat	gagtctagaa	taaagattgc	atcttgtgtt	tctattcaag	aatagtggat	6420
aggaatggct	atttaacaat	tcaaaaataa	tccgaaaagca	gtggtgaaaa	tcattgcttt	6480
cagttgcttt	ctttgtactt	tagtgcttaa	atataatata	ctaaagttat	ggaatttatg	6540
agaaaggaat	ttcacaacgt	tttatctagt	ggtcagttgc	ttgcagacaa	aaggccagca	6600
agagactata	atagaaaata	gggtaggtat	ttattctaag	aaaaataaaa	aatagagagc	6660
agttaaaagta	tgaaaatttt	aattgtagaa	gatgaagaga	tgatccgtga	gggggtcagt	6720
gattatttga	cggattgtgg	ctatgaaact	attgaggcag	cggacggtca	ggaagctctg	6780
gagcaatttt	ctagctatga	ggtggccctg	gttttactgg	atatccagat	gcccagctc	6840
aacggcttag	aagtcctagc	tgagattcgt	aaaaccagtc	aggttcctgt	cttgatgttg	6900
acagcttttc	aagatgagga	atacaagatg	agtgcccttg	cctctttggc	agatggctat	6960
ctggaaaaaac	ctttctccct	ctccctttta	aaagtgaggg	tggacgcgat	tttcaagcgc	7020
tactacgata	caggacgaat	cttttcttac	aaggatacca	aggtggactt	tgaaagctac	7080
agtgcagacc	tcgcaggtca	agaagtgcct	atcaatgcca	aagagttgga	aattctggac	7140
tatctagtga	aaaatgaagg	ccgggccttg	actcgatctc	agattatcga	tgccgtctgg	7200
aaagcgacag	atgaggttcc	ctttgaccgt	gttattgatg	tttatatcaa	ggaattgcgg	7260
aaaaagctag	acttgatttg	tatcctcact	gtgcgcaatg	ttggttataa	attggagcga	7320
aaatgaaacg	aacaggttta	tttgcaaaga	tatttatcta	taccttctcg	atatttagtg	7380
ttctggttat	ctgccttcat	ttagctatct	atcttctttt	tccttcgact	tatctgagtc	7440
atcgctcagga	aaccattggg	caaaaggcaa	cagccattgc	ccagtcctta	gaagggaag	7500
ataggcagag	tatcgagcaa	gtgttagact	tgtattccca	gactagtgat	atcaagggga	7560
ccgtcaaagg	tgagatgacc	gaggacaagt	tagaagtcaa	ggacagtctt	cctctggaca	7620
cagaccgcca	gacaacctct	ctctttattg	aggagcgca	ggtgaaaacg	caagacggtg	7680
gtactatgat	tctccagttt	ctagcttcca	tggatttaca	aaaggaagcg	gagcaaatca	7740
gtctccagtt	tcttccttat	accttgctgg	cctcctttct	gatttccttt	ttggtggcct	7800
acatctacgc	tcggactatt	gttgcaaccg	ttttggaaat	caagcgggtg	acccgtcgga	7860
tgatggacct	ggattcccaa	gtgcgattgc	gcgtggattc	taaggatgag	ataggtaatc	7920
tcaaggaaca	aatcaatagc	ctctaccagc	atctcttgac	tgttattgcg	gacttgcatg	7980
aaaagaatga	agccattctc	cagctggaga	agatgaaggt	cgaattccta	cgaggagctt	8040
ctcatgaatt	gaaaacaccg	ctggctagtt	tgaaaatcct	aatcgaaaat	atgagagaga	8100
atatcggtcg	ttataaggat	agagaccagt	atctgggagt	tgcttggggg	attgtggatg	8160

aactcaatca ccatgttctg cagatacttt ccctctcttc tgtgcaggaa ttgcgagatg 8220
atagggaaac aattgacctc ctccagatga cgcaaatct ggtcaaagat tatgccttgc 8280
tagccaagga aagagagctc cagatagaca atagtttgac ccatcagcag gcttatctaa 8340
acccatcagt tatgaagttg attctttcta atctcatcag caatgccatt aagcactctg 8400
ttccaggtgg cttagttcga attggagaaa gagaaggaga actttttatc gaaaatagct 8460
gtagctcaga ggaacaagaa aaactagccc agtctttttc tgacaatgcc agtcgcaagg 8520
tcaaggggtc tggatatggg ctctttgtgg ttaagagtct attagaacat gaaaaattag 8580
cttatcgttt cgagatggag gagaatagtt taaccttctt tatagatttt ccaaaagtcg 8640
tccaagacta gggagagaaa gggtttacat agatggagtt agaagaaaat caatcgaaac 8700
tgcgggaaaa actagatttt tttggcaaaa agtgataaaa tgaacaatgt aaatgggatg 8760
accataaaa atatacagga ggcctgataa aatggcaatc gtttcagcag aaaaatttgt 8820
ccaagcagcc cgtgacaacg gttatgcagt tgggtgattt aacacaaaac accttgagtg 8880
gactcaagct atcttgcgcg 8900

<210> 26
<211> 25
<212> PRT
<213> bacterial

<400> 26
Asn Arg Lys Val Phe Ile Val Val Leu Ser Met Leu Leu Leu Leu Ala
1 5 10 15

Met Glu Arg Pro Trp Cys Ser Leu Val
20 25

<210> 27
<211> 25
<212> PRT
<213> bacterial

<400> 27
Ser Ser Leu Leu Asp Gly Val Lys Ile Ala Ser Gly Asn Leu Leu Ala
1 5 10 15

Ser Thr Lys Pro Ser Gly Asn Phe Asn
20 25

<210> 28
<211> 25
<212> PRT
<213> bacterial

<400> 28
Ser Arg Lys Arg Phe His Gln Ile Leu Met Gln Gly Met Lys Leu Ala
1 5 10 15

<400> 32

Arg Cys Leu Arg Arg Asp Ser Leu Phe Ser Ser Gly Cys Leu Leu Ala
1 5 10 15

Gly Glu Glu Pro Ser Arg Arg Ser Cys
20 25

<210> 33

<211> 25

<212> PRT

<213> bacterial

<400> 33

Val Leu Arg Thr His Gly Thr Val Leu Ser Ala Lys Gln Leu Ile Asn
1 5 10 15

Ala Lys Asn Pro Ser Arg Tyr Phe Gly
20 25

<210> 34

<211> 20

<212> PRT

<213> bacterial

<400> 34

Leu Lys Glu Glu Phe Glu Lys Phe Arg Ser Ala Gly Glu Lys Leu Leu
1 5 10 15

Asp Phe Arg Pro
20

<210> 35

<211> 12

<212> PRT

<213> bacterial

<400> 35

Phe Gly Asn Gln Leu Ser Ile Gly Gln Leu Ile Ala
1 5 10

<210> 36

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 36

Met Arg Lys Glu Phe His Asn Val Leu Ser Ser Gly Gln Leu Leu Ala
1 5 10 15

Asp Lys Arg Pro Ala Arg Asp Xaa Asn
20 25

<210> 37

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 37

aatgagtcta gaataaagat tgc 23

<210> 38

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 38

tcttagaata aatacctacc c 21

<210> 39

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 39

Arg Lys Glu Phe His Xaa Xaa Xaa Xaa Xaa Xaa Gln Leu Leu Xaa Asp
1 5 10 15

Lys Arg Pro Xaa Arg Asp Tyr

<210> 40
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 40
 Asp Lys Arg Pro Ala Arg Asp Tyr
 1 5

<210> 41
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 41
 Arg Lys Glu Phe His Asn Val
 1 5

<210> 42
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 42
 Leu Ser Ser Gly Gln Leu Leu
 1 5

<210> 43
 <211> 25
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 43

Met Xaa Xaa Xaa Xaa Xaa Asn Val Leu Ser Xaa Gly Xaa Xaa Xaa Ala
1 5 10 15

Xaa Xaa Xaa Xaa Ala Xaa Xaa Xaa Asn
20 25

<210> 44

<211> 27

<212> PRT

<213> bacterial

<400> 44

Met Arg Lys Glu Phe His Asn Val Leu Ser Ser Gly Gln Leu Leu Ala
1 5 10 15

Asp Lys Arg Pro Ala Arg Asp Tyr Asn Arg Lys
20 25

<210> 45

<211> 312

<212> DNA

<213> bacterial

<400> 45

aatttgaaaa aatgagtcta gaataaagat tgcattcttgt gtttctattc aagaatagtg 60
gataggaatg gctattttaac aattcaaaat aaatccgaaa gcagtggatg aaatcattgc 120
tttcagttgc tttctttgta ctttagtgct taaatataat atactaaagt tatggaattt 180
atgagaaagg aatttcacaa cgttttatct agtggtcagt tgcttgacaga caaaaggcca 240
gcaagagact ataatagaaa atagggtagg tattttattct aagaaaaata aaaaatagag 300
agcagttaaa gt 312

<210> 46

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 46

aatgagtcta gaataaagat tgc 23

<210> 47

attaaggatc cagctatcaa

20

<210> 51

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 51

atcaagggat ccactgcaa ggc

23

<210> 52

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 52

agaggagaat tcccacttcc ttgcg

25

<210> 53

<211> 81

<212> DNA

<213> bacterial

<400> 53

atgagaaagg aatttcacaa cgttttatct agtggtcagt tgcttgaga caaaaggcca 60
gcaagagact ataataaaaa a 81

<210> 54

<211> 90

<212> DNA

<213> bacterial

<400> 54

atggaattta tgagaaagga atttcacaac gttttatcta gtggtcagtt gcttgagac 60
aaaaggccag caagagacta taatagaaaa 90